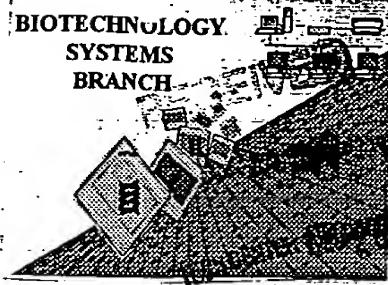


*January*

## RAW SEQUENCE LISTING ERROR REPORT



TECH CENTER 1800/8906

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/424,482

Source: 1627

Date Processed by STIC: 12/11/2005

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin30help@uspto.gov](mailto:patin30help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/424,482

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1  Wrapped Nucleic The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

2  Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".

3  Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.

4  Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5  Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6  Variable Length Sequence(s) 4-5 (maybe more) contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.

7  PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

8  Skipped Sequences (OLD RULES) Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X:  
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9  Skipped Sequences (NEW RULES) Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000

10  Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11  Use of <213>Organism (NEW RULES) Sequence(s)        are missing this mandatory field or its response.

12  Use of <220>Feature (NEW RULES) Sequence(s)        are missing the <220>Feature and associated headings.  
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)

13  PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.

1627

Does Not Comply  
Corrected Diskette Needed

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,482

DATE: 12/11/2000  
TIME: 16:39:46

Input Set : A:\CHOO 424482 SEQUENCE.txt  
Output Set: N:\CRF3\12112000\I424482.raw, ..

PP 523

3 <110> APPLICANT: Medical Research Council  
4 Choo, Yen  
5 Klug, Aaron  
6 Isalan, Mark  
8 <120> TITLE OF INVENTION: Nucleic Acid Binding Polypeptide Library  
10 <130> FILE REFERENCE: 71278/264974  
12 <140> CURRENT APPLICATION NUMBER: US 09/424,482  
C--> 13 <141> CURRENT FILING DATE: 2000-02-29  
15 <150> PRIOR APPLICATION NUMBER: GB9710809.6  
16 <151> PRIOR FILING DATE: 1997-05-23  
18 <150> PRIOR APPLICATION NUMBER: PCT/GB98/01510  
19 <151> PRIOR FILING DATE: 1998-05-25  
21 <160> NUMBER OF SEQ ID NOS: 19  
23 <170> SOFTWARE: PatentIn version 3.0  
25 <210> SEQ ID NO: 1  
26 <211> LENGTH: 9  
27 <212> TYPE: DNA  
28 <213> ORGANISM: Artificial  
30 <220> FEATURE:  
31 <223> OTHER INFORMATION: Description of Artificial Sequence: LIB-A DNA sorting sequence  
33 <220> FEATURE:  
34 <221> NAME/KEY: variation  
35 <222> LOCATION: (2)..(4)  
36 <223> OTHER INFORMATION: n is any nucleotide  
39 <400> SEQUENCE: 1  
OK> 40 gnnnccggcg 9  
43 <210> SEQ ID NO: 2  
44 <211> LENGTH: 9  
45 <212> TYPE: DNA  
46 <213> ORGANISM: Artificial  
48 <220> FEATURE:  
49 <223> OTHER INFORMATION: Description of Artificial Sequence: LIB-B DNA sorting sequence  
51 <220> FEATURE:  
52 <221> NAME/KEY: variation  
53 <222> LOCATION: (3)..(4)  
54 <223> OTHER INFORMATION: n is any other nucleotide  
57 <400> SEQUENCE: 2  
OK> 58 gcnnccggcg 9  
61 <210> SEQ ID NO: 3  
62 <211> LENGTH: 9  
63 <212> TYPE: DNA  
64 <213> ORGANISM: Artificial  
66 <220> FEATURE:  
67 <223> OTHER INFORMATION: Description of Artificial DNA: LIB 1/2 sorting sequence  
69 <220> FEATURE:  
70 <221> NAME/KEY: variation  
71 <222> LOCATION: (5)..(9)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,482

DATE: 12/11/2000  
TIME: 16:39:46

Input Set : A:\CHOO 424482 SEQUENCE.txt  
Output Set: N:\CRF3\12112000\I424482.raw

72 <223> OTHER INFORMATION: n is any other nucleotide  
 75 <400> SEQUENCE: 3  
 76 gcggnnnnn  
 79 <210> SEQ ID NO: 4  
 80 <211> LENGTH: 18  
 81 <212> TYPE: PRT  
 82 <213> ORGANISM: Artificial  
 84 <220> FEATURE:  
 85 <223> OTHER INFORMATION: Description of Artificial Sequence: Structure A  
 87 <220> FEATURE:  
 88 <221> NAME/KEY: SITE  
 89 <222> LOCATION: (1)..(1)  
 90 <223> OTHER INFORMATION: Xaa is any amino acid  
 93 <220> FEATURE:  
 94 <221> NAME/KEY: SITE  
 95 <222> LOCATION: (3)..(3)  
 96 <223> OTHER INFORMATION: Xaa is any amino acid  
 99 <220> FEATURE:  
 100 <221> NAME/KEY: SITE  
 101 <222> LOCATION: (5)..(13)  
 102 <223> OTHER INFORMATION: Xaa is any amino acid  
 105 <220> FEATURE:  
 106 <221> NAME/KEY: SITE  
 107 <222> LOCATION: (15)..(17)  
 108 <223> OTHER INFORMATION: Xaa is any amino acid  
 111 <220> FEATURE:  
 112 <221> NAME/KEY: VARIANT  
 113 <222> LOCATION: (1)..(1)  
 114 <223> OTHER INFORMATION: 0 - 2 possible residues  
 117 <220> FEATURE:  
 118 <221> NAME/KEY: VARIANT  
 119 <222> LOCATION: (3)..(3)  
 120 <223> OTHER INFORMATION: 1 - 5 possible residues  
 123 <220> FEATURE:  
 124 <221> NAME/KEY: VARIANT  
 125 <222> LOCATION: (5)..(13)  
 126 <223> OTHER INFORMATION: 9 - 14 possible residues  
 129 <220> FEATURE:  
 130 <221> NAME/KEY: VARIANT  
 131 <222> LOCATION: (15)..(17)  
 132 <223> OTHER INFORMATION: 3 - 6 possible residues  
 135 <220> FEATURE:  
 136 <221> NAME/KEY: SITE  
 137 <222> LOCATION: (18)..(18)  
 138 <223> OTHER INFORMATION: X is His or Cys  
 141 <400> SEQUENCE: 1  
 W--> 143 Xaa Cys Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa His Xaa Xaa 10 15  
 144  
 W--> 146 Xaa Xaa

variable length is  
not permitted  
(see item 6 on  
Error Summary  
sheet)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,482

DATE: 12/11/2000  
TIME: 16:39:46

Input Set : A:\CHOO 424482 SEQUENCE.txt  
Output Set: N:\CRF3\12112000\I424482.raw

149 <210> SEQ ID NO: 5  
 150 <211> LENGTH: 21  
 151 <212> TYPE: PRT  
 152 <213> ORGANISM: Artificial  
 154 <220> FEATURE:  
 155 <223> OTHER INFORMATION: Description of Artificial Sequence: Structure B  
 157 <220> FEATURE:  
 158 <221> NAME/KEY: SITE  
 159 <222> LOCATION: (1)..(1)  
 160 <223> OTHER INFORMATION: Xaa is any amino acid  
 163 <220> FEATURE:  
 164 <221> NAME/KEY: SITE  
 165 <222> LOCATION: (3)..(4)  
 166 <223> OTHER INFORMATION: Xaa is any amino acid  
 169 <220> FEATURE:  
 170 <221> NAME/KEY: SITE  
 171 <222> LOCATION: (6)..(7)  
 172 <223> OTHER INFORMATION: Xaa is any amino acid  
 175 <220> FEATURE:  
 176 <221> NAME/KEY: SITE  
 177 <222> LOCATION: (9)..(13)  
 178 <223> OTHER INFORMATION: Xaa is any amino acid  
 181 <220> FEATURE:  
 182 <221> NAME/KEY: SITE  
 183 <222> LOCATION: (15)..(16)  
 184 <223> OTHER INFORMATION: Xaa is any amino acid  
 187 <220> FEATURE:  
 188 <221> NAME/KEY: SITE  
 189 <222> LOCATION: (18)..(20)  
 190 <223> OTHER INFORMATION: Xaa is any amino acid  
 193 <220> FEATURE:  
 194 <221> NAME/KEY: VARIANT  
 195 <222> LOCATION: (3)..(4)  
 196 <223> OTHER INFORMATION: 2 or 0 amino acids  
 199 <220> FEATURE:  
 200 <221> NAME/KEY: VARIANT  
 201 <222> LOCATION: (6)..(7)  
 202 <223> OTHER INFORMATION: 2 or 0 amino acids  
 205 <420> SEQUENCE 5  
 W--> 207 Xaa Cys Xaa Xaa Cys Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa  
 208 1 / 5 10 15  
 W--> 210 His Xaa Xaa Xaa His  
 211 20  
 213 <210> SEQ ID NO: 6  
 214 <211> LENGTH: 4  
 215 <212> TYPE: PRT  
 216 <213> ORGANISM: Artificial  
 218 <220> FEATURE:  
 219 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker

variable length is not permitted  
 (see item 6 on  
 Error Summary  
 Sheet)

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,482

DATE: 12/11/2000  
TIME: 16:39:46

Input Set : A:\CHOO 424482 SEQUENCE.txt  
Output Set: N:\CRF3\12112000\I424482.raw

221 <400> SEQUENCE: 6  
223 Thr Gly Glu Lys  
224 1  
226 <210> SEQ ID NO: 7  
227 <211> LENGTH: 5  
228 <212> TYPE: PRT  
229 <213> ORGANISM: Artificial  
231 <220> FEATURE:  
232 <223> OTHER INFORMATION: Description of Artificial Sequence: Linker  
234 <400> SEQUENCE: 7  
236 Thr Gly Glu Lys Pro  
237 1 5  
239 <210> SEQ ID NO: 8  
240 <211> LENGTH: 26  
241 <212> TYPE: PRT  
242 <213> ORGANISM: Artificial  
244 <220> FEATURE:  
245 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus structure  
247 <400> SEQUENCE: 8  
249 Pro Tyr Lys Cys Pro Glu Cys Gly Lys Ser Phe Ser Gln Lys Ser Asp  
250 1 5 10 15  
252 Leu Val Lys His Gln Arg Thr His Thr Gly  
253 20 25  
255 <210> SEQ ID NO: 9  
256 <211> LENGTH: 29  
257 <212> TYPE: PRT  
258 <213> ORGANISM: Artificial  
260 <220> FEATURE:  
261 <223> OTHER INFORMATION: Description of Artificial Sequence: Consensus structure  
263 <400> SEQUENCE: 9  
265 Pro Tyr Lys Cys Ser Glu Cys Gly Lys Ala Phe Ser Gln Lys Ser Asn  
266 1 5 10 15  
268 Leu Thr Arg His Gln Arg Ile His Thr Gly Glu Lys Pro  
269 20 25  
271 <210> SEQ ID NO: 10  
272 <211> LENGTH: 6  
273 <212> TYPE: PRT  
274 <213> ORGANISM: Artificial  
276 <220> FEATURE:  
277 <223> OTHER INFORMATION: Description of Artificial Sequence: Leader peptide  
279 <400> SEQUENCE: 10  
281 Met Ala Glu Glu Lys Pro ..  
282 1 5  
284 <210> SEQ ID NO: 11  
285 <211> LENGTH: 9  
286 <212> TYPE: DNA  
287 <213> ORGANISM: Artificial  
289 <220> FEATURE:  
290 <223> OTHER INFORMATION: Description of Artificial DNA: LIB 2/3 DNA sorting sequence

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/424,482

DATE: 12/11/2000  
TIME: 16:39:46

Input Set : A:\CHO0 424482 SEQUENCE.txt  
Output Set: N:\CRF3\12112000\I424482.raw

RECEIVED

DEC 26 2000

TECH CENTER 1600/2900

292 <220> FEATURE:  
293 <221> NAME/KEY: variation  
294 <222> LOCATION: (1)..(5)  
295 <223> OTHER INFORMATION: n is any nucleotide  
298 <400> SEQUENCE: 11  
OK > 299 nnnnnngcg  
302 <210> SEQ ID NO: 12  
303 <211> LENGTH: 9  
304 <212> TYPE: DNA  
305 <213> ORGANISM: Artificial  
307 <220> FEATURE:  
308 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger -DNA interaction  
309 sequence  
311 <400> SEQUENCE: 12  
312 cgccccacgc  
315 <210> SEQ ID NO: 13  
316 <211> LENGTH: 9  
317 <212> TYPE: DNA  
318 <213> ORGANISM: Artificial  
320 <220> FEATURE:  
321 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger-DNA interaction s move  
322 Sequence down  
324 <400> SEQUENCE: 13  
325 acgccccacg  
328 <210> SEQ ID NO: 14  
329 <211> LENGTH: 9  
330 <212> TYPE: DNA  
331 <213> ORGANISM: Artificial  
333 <220> FEATURE:  
334 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger-DNA interaction s  
335 Sequence  
337 <400> SEQUENCE: 14  
338 gcggtggcg  
341 <210> SEQ ID NO: 15  
342 <211> LENGTH: 9  
343 <212> TYPE: DNA  
344 <213> ORGANISM: Artificial  
346 <220> FEATURE:  
347 <223> OTHER INFORMATION: Description of Artificial Sequence: Zinc finger-DNA interaction 1  
348 library designed sequence  
350 <220> FEATURE:  
351 <221> NAME/KEY: variation  
352 <222> LOCATION: (7)..(9)  
353 <223> OTHER INFORMATION: n is any nucleotide  
356 <400> SEQUENCE: 15  
OK > 357 acgccccnn  
360 <210> SEQ ID NO: 16  
361 <211> LENGTH: 36  
362 <212> TYPE: PRT  
9

FYI

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY DATE: 12/11/2000  
PATENT APPLICATION: US/09/424,482 TIME: 16:39:47

Input Set : A:\CHOO 424482 SEQUENCE.txt  
Output Set: N:\CRF3\12112000\I424482.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:40 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#1  
L:58 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#2  
L:76 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#3  
L:143 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#4  
L:146 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#4  
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#5  
L:210 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#5  
L:299 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#11  
L:357 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#15  
L:400 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#17  
L:425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#18  
L:447 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#19